

Figure 1.

CCCCGTCGGAGGTTTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGAC 60  
AAGGTGATGGTTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTCCAGCCTTAAT 120  
AATTCATGAATTCTGTAATTTTATTCTTGATCTTTTTGAGCGAAGTTTGTGGGGATT 180  
TTAGTTTGGTTTCCCTGTCACGTGTTTTCTTCCCTGAAACTGACTTTCATTTGCAACATG 240  
AGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCAATGGCTGCTTAGAAGTAGTGAGAAA 300  
CATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTGCCAAACTGTAGCTTTGGG 360  
ATTTGAGGAGCCACAGAGTTGTATATAAAATTTGTTTAATGATATCCTGCCCCCTGCCTTCC 420  
ATTAATTGCTTGTTTTATGAAACCACTCTTTTTTTTTTTTTTTTTTTTGGCTTCTTCA 480  
TATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGG 540  
ATGACAGTGGTACAGGAGCTCTGAATTTTTTAGATAAACTATGAGAGTGGAAACAGAAAT 600  
CTGAGGCTAGTTTCTTGAGCTGACTGTAAATTTTGTGAGAATATTTTCAAGACTACATTA 660  
GTTGTGTGTTTGAGGAAAAATAAAATGTTTAAGTTGTCCATTCCTTGAAACCTCCCGACC 720  
GGG 723

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Figure 2.

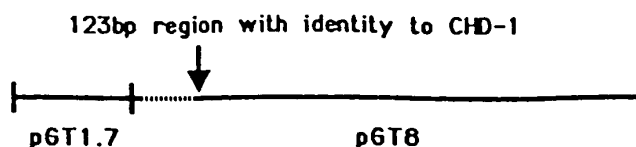


Figure 3.

M	CHD-1	ATTCTTCAG	ATGATCCTGA	TAAAAAACCA	CAAGCAAAAC	AGTTACAGAC
C	CHD-1A	ATTTTACCTG	ATGATCCAGA	CAAGAAACCC	CAGGCAAAGC	AGCTACAGAC
C	CHD-W	ATTTTACCTG	ATGATCCAGA	TAAGAAACCC	CAGGCTAAGC	AGTTACAGAC
GT	CHD-W	ATTTTACCTG	ATGACCCAGA	TAAGAAACCA	CAGGCAAAGC	AGTTGCAGAC
M	CHD-1	CAAAAAACCA	CAAGCAAAAC	AGTTACAGAC	CCGTGCAGAC	TACCTCATCA
C	CHD-1A	CAAGAAACCC	CAGGCAAAGC	AGCTACAGAC	CCGTGCAGAC	TACCTCATTA
C	CHD-W	CAAGAAACCC	CAGGCTAAGC	AGTTACAGAC	CCGTGCAGAT	TACCTCATTA
GT	CHD-W	CAAGAAACCA	CAGGCAAAGC	AGTTGCAGAC	CCGTGCAGAT	TACCTCATTA
M	CHD-1	AACTACTTAG	CAGAGATCTT	GCAAAAAGAG	AGGCTCAGAG	ACTTGCTGGT GCG
C	CHD-1A	AATTACTGAA	TAAAGACCTT	GCAAGAAAGG	AAGCACAAAG	GCTTGCTGGT GCA
C	CHD-W	AATTACTGAA	TAAAGACCTT	GCAAGAAAGG	AAGCACAGAG	ACTTGCTGGT GCA
GT	CHD-W	AATTACTGAA	TAAAGACCTT	GCAAGAAAGG	AAGTGCAAAG	ACTTACTGGT GCA
M	CHD-1	ILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREAQRLCGA				
C	CHD-1A	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA				
C	CHD-W	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA				
GT	CHD-W	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEVQRLTGA				
		*****				

Figure 4.



Figure 5.

1 CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG  
 51 AAGGCCTGGC CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT  
 101 TGGCCATCTG TAGAGAATAG CAAGTCAAAC GCATTACTTC GAAAAACATAC  
 151 GGAGTACCAG AAAGGGGATT CTTGACCTAC ACCTTGTAAC CTGAGTGGAC  
 201 TTTCTTTTAA ACTTCTTAAT ACTTACAATG AATGGGCACA GTGATGAAGA  
 251 AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG  
 301 GGTCAGCTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT  
 351 GGAAGTAGCA GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC  
 401 AGGCAGTCAA TCCGAATCAG AGTCTGACAC ATCTAGAGAG AAGAAACAAG  
 451 TTCAAGCTAA ACCTCCGAAA GCTGACGGAT CTGAGTTTGT GAAGTCCAGT  
 501 CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA AGCAACAGCA  
 551 ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA  
 601 GTAGTGAAGA TTCTGCCGAT GATTCTGTCCA GTGAACTAA GAAGAAAAAG  
 651 CATAAAGATG AAGACTGGCA AATGTCTAGG TCAGGGTCAG TATCAGGAAC  
 701 TGGTTCTGAT TCTGAATCGG CGGAAGATGG GGATAAAAGC AGTTGTGAAG  
 751 AAAGTGAATC TGACTATGAG CCAAAAAACA AAGTCAAAAG CCGTAAACCT  
 801 CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG GACAGAAGAA  
 851 GAGGCAACTT GATTTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG  
 901 ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA  
 951 GCTGAAGAAA CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA  
 1001 GGATGTCCCA CAGACTGAAG AAGATGAATT TGAAACTATA GAGAAGTTTA  
 1051 TGGACAGTCG AATTGCGCGA AAAGGAGCCA CTGGTGCCTC AACCACCATC  
 1101 TATGCCGTTG AGGCAGATGG TGACCCAAAT GCTGGGTTTG AAAAGTCAAA  
 1151 GGAGCTGGGA GAAATACAGT ATCTTATTAA ATGGAAAGGC TGGTCACACA  
 1201 TCCATAACAC TTGGGAAACT GAAGAAACGC TGAAGCAACA AAATGTTAAA  
 1251 GGAATGAACA AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG  
 1301 CTGGCTGAAA AATGCTTCTC CAGAAGATGT GGAATATTAT AACTGCCAGC  
 1351 AGGAGCTTAC AGATGATCTG CACAAACAAT ATCAAATAGT GGAAGAATA  
 1401 ATTGCTCATT CAAATCAAAA GTCAGCAGCT GGTATCCGG ACTACTATTG  
 1451 CAAATGGCAG GGTCTGCCTT ACTCAGAATG TAGCTGGGAA GATGGTGCTC  
 1501 TCATTGCCAA AAAGTTTCAG GCACGCATTG ATGAGTATTT TAGCAGAAAT  
 1551 CAATCCAAGA CTAATCCCTT TAAGGACTGC AAGGTTCTAA AACAGAGACC  
 1601 AAGATTTGTT GCACTGAAGA AGCAACCATC TTACATTGGA GGACATGAAA  
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 1701 TCATGGTGCA AAGGAAATAG TTGTATTCTT GCAGATGAAA TGGGTCTGGG  
 1751 TAAAACAATA CAAACAATTT CTTTCTGAA CTACCTGTTT CATGAACATC  
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 2001 ATTTTACTGA AGGATAAGTC ATTCCTTGGT GGTCTCAATT GGCATTTCAT  
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 2101 GGACTTTAAT AGACTTTAAG TCCAACCATC GACTTCTGAT TACTGGAACC  
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 2201 GCCAGAAAAA TTTTCTCCTT GGAAGATTTT TGAAGAGGAG CATGGCAAAG  
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 2501 TTGCTACCTC ATTAAGCCAC CAGATGATAA TGAATTCTAT AATAAACAGG  
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 2601 AAGCTACTGA TTCGTCTGCG AGAACGTGGC AACAGAGTTC TGATTTTCTC  
 2651 TCAGATGGTG AGGATGCTGG ACATCCTAGC AGAATATCTG AAGTATCGCC  
 2701 AGTTTCCCTT CCAGAGACTT GATGGATCAA TAAAAGGGGA ATTGAGGAAG  
 2751 CAAGCACTGG ATCATTTCAA TGCAGAAAGG TCAGAGGATT TCTGTTTTTT  
 2801 ACTGTCTACA AGAGCTGGAG GATTAGGTAT TAACTTGGCA TCTGCTGACA  
 2851 CTGTAGTTAT TTTTGATTCT GACTGGAATC CACAGAATGA TCTGCAGGCA  
 2901 CAGGCGAGAG CTCATAGAAT TGGACAGAAG AAACAGGTTA ATATTATCG  
 2951 GCTAGTCACA AAAGATCAG TAGAAGAAGA TATTCTTGAA AGAGCCAAGA

3001 AGAAGATGGT GCTAGACCAT TTAGTAATTC AGAGAATGGA CACGACAGGA  
 3051 AAAACTGTTC TGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTTAA  
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 3151 AAGAACCTGA AGGAGAAGAA CAGGAGCCCC AGGAAATGGA TATAGATGAA  
 3201 ATCTTGAAGA GAGCTGAAAC TCGGGAAAAT GAGCCAGGTT CATTGACTGT  
 3251 AGGGGATGAG TTGCTTTTAC AGTTCAAGGT GGCAGAACTTT TCCAATATGG  
 3301 ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTC AAG AAATTGGGAA  
 3351 GAAATCATCC CAGAATCCCA ACGGAGAAGG ATAGAGGAGG AGGAAAGACA  
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 3451 AACAGATCAG CTTTAATGGG AGTGAAGGAA GACGCAGTAG GAGCAGAAGA  
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 3751 AGGCTTTAAA GGACAATTCA TCTGGACAAG AAAGAGCAGG AGGTAGACTT  
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4351 TGAAATCTGA AAATAAAGAA AAATCTAAAA AAATTCATT GCTGGATACT  
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 4451 TGAAGAACTC CATCAGAAGA CATTTAGTGT GTGCAAAGAA AGAATGAGGC  
 4501 CTGTCAAAGC AGCACTGAAA CAGCTGGATA GACCAGAGAA GGGCCTTTCT  
 4551 GAAAGGGAGC AGCTGGAACA TACTAGGCAG TGTCTAATCA AAATTGGGGA  
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 4651 AGTGGAGGAA AAATTTGTGG ATTTTGTGT CCAAGTTTAC AGAATTTGAT  
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 6301 TGATTGTTGT AATGAACAGT GAGAATATCC CACTCTAAAC TGTGCCCTGG  
 6351 AAAGCTTTTC AGGTGCATTG GTTTAAAGA AGGAAGTGT TATAGGTGA

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6401  ACACTTCAA ACCCAGATCA GCCAAGATTC ATTGTAAATC CATTGTGTTT
6451  CCCTCTTTAA CATGGGCAAT AATGTCAAAT GTGCTATGCA GCAGTTAATA
6501  TTTTAGAAGA TTTGAATGAC TTTATTAACA GAATTGTTAC AATGCACACT
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6601  AAAAAACC

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Figure 6.

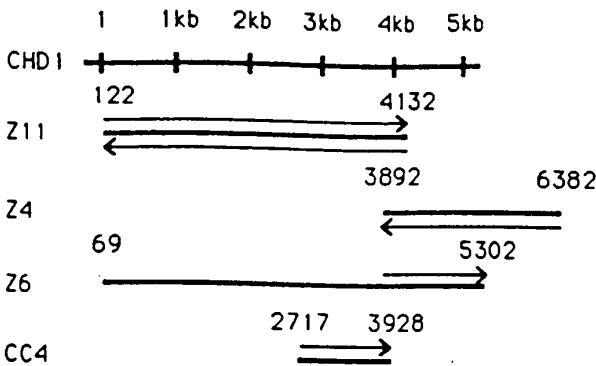


Figure 7.

		D E I V S V K H L H K K I K T E
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CHD-W	1	GATGGGATTGTTTCAGTGAACATCCACATAAAAAAATAAAAGCAGAAA
		D G I V S V K H P H K K I K A E
		K E N E E K P E P D I G I K K E A
CHD-1A	51	AAAGAAAATGAAGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCT
CHD-W	51	AAAGAAAATGAAGAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCT
		K E N E E K D E P E I G I K K E A
		E E K R E T K E K E N K R E L K R
CHD-1A	101	GAAGAAAAAGAGAGACAAAAGAGAAGGAAATAAAAGGGAATTGAAAAGG
CHD-W	101	GGAGAAAAAGAGAGACAAAAGAAAAGGAAATAAGA
		G E K R E T K E K E N K
		E K K E K E D K K E L K E K D N K
CHD-1A	151	GAGAAAAAGAAAAAGAGGATAAGAAAGAATTAAAGAAAAAGATAATAAA
		E K R E N K V K E S T Q K E K E V
CHD-1A	201	GAAAAGAGAGAAAAACAAAGTAAAGAATCCACACAGAAAAGAAAAGGAAGTG
		K E E K
CHD-1A	251	AAGGAAGAGAAG

Figure 8.

ATTTATCGGC	TAGTCACAAA	AGGATCAGTA	GAAGAAGATA	TTCTTGAAAG	AGCCAAGAAA	AAGATGGTGT	TAGATCATTT
10	20	30	40	50	60	70	80
AGTGATTCAG	AGAATGGACA	CCACAOGGAA	AACTGTACTA	CATACAGGCT	CTACTCCTTC	AAGCTCAACA	CCTTTTAATA
90	100	110	120	130	140	150	160
AGGAAGAGTT	ATCAGCAATT	TTGAAGTTTG	GTGCTGAGGA	ACTTTTITAAA	GAACCTGAAN	NNGAAGAAGA	GGAGCCTCAG
170	180	190	200	210	220	230	240
GAGATGGATA	TAGATGAAAT	CCTGAAGAGG	NCTGAAACTC	GAGAAAATGA	GTCAGGCCCA	TTAAGTGTAG	GAGATGAGTT
250	260	270	280	290	300	310	320
ACTTTTCACAG	TTCAAGGTAG	CTAACTTTTC	CAATATGGAT	GAAGATGACA	TTGAATTGGA	ACCAGAACAA	AATCTAAGAA
330	340	350	360	370	380	390	400
ACTGGGAAGA	AATCATTCOA	GAAGTTCAGT	GGCGACGAAT	AGAGGGGNG	GAAAGACAAA	AAGAAGTTGA	AGAAATATAT
410	420	430	440	450	460	470	480
ATGCTTCCAA	GAATGAGAAA	CTGTGCAAAA	CAGATCAGCT	TTAATGGAAA	TGAAGGGAGA	TGCAGTAGGA	GCAGAAGATA
490	500	510	520	530	540	550	560
TTCTGGATCT	GATAGTGATT	CCATCTCAGA	AAGAAAACGA	CCAAAAAAC	GTGGACGACC	ACGAAGTATT	CCCCGTGAAA
570	580	590	600	610	620	630	640
ACATTAAAGG	ATTTAGTGAT	GCAGAGATTA	GACGATTAT	CAAGAGTTAC	AAGAAATTTG	GTGGCCCACT	TGAAAGGTTA
650	660	670	680	690	700	710	720
GATGCTATAG	CTAGAGATGC	TGAGCTAGTT	GATAAATCTG	AAACAGACCT	TAGACGTCTG	GGAGAAGTTG	TACATAATGG
730	740	750	760	770	780	790	800
ATGCATTAAG	GCTTTAAATG	ATAATGACTT	TGGTCAAGGA	AGAACAGGTG	GTAGATTTGG	GAAAGTTAAA	GGCCCAACAT
810	820	830	840	850	860	870	880
TCCGAATAGC	AGGAGTGCAG	GTGAATGCAA	AGCTAGTCAT	TTCTCACGAA	GAAGAGTTGG	CACCATTGCA	TAAATCGATT
890	900	910	920	930	940	950	960
CCTTCAGATC	CAGAAGAAAG	GAAGAGATAT	GTCAATCCAT	ACCACACCAA	AGCAGCTCAT	TTTGATATAG	ATTGGGGTAA
970	980	990	1000	1010	1020	1030	1040
AGAAGATGAT	TCCAATCTGT	TAATAGGCAT	CTATGAATAT	GGTTATGGCA	GTGGGAAAT	GATAAAATG	GATCCTGATC
1050	1060	1070	1080	1090	1100	1110	1120
TCAGTTTGAC	ACAGAAGATT	TTACCTGATG	ATCCAGATAA	GAAACCCAG	GCTAAGCAGT	TACAGACTCG	TGCAGATTAC
1130	1140	1150	1160	1170	1180	1190	1200
CTCATTAAT	TACTGAATAA	AGACCTTGCA	AGAAAGGAAG	CACAGAGACT	TGCTGGTGCA	GGCAATTCAA	AGAGGAGAAA
1210	1220	1230	1240	1250	1260	1270	1280
AACAAGAAGT	AAGAAGAATA	AAGCAACAAA	GGCTGC				
1290	1300	1310					

664020" 69224680



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Figure 9.

Sheet 2 of 2

C CHD-1A	DARRYLGNLHGL*RIASQTHYFENIRSTRKGILDLELVT*VDFLNFILITMNGHSDEE
M CHD-1	FALCPFVTQREPQETRECRKFIFEILIFEICIEHLLIGDFCFINFLIPTMNGHSDEE
	*****
C CHD-1A	SVRNSSGESRSDDDSAGSASGSGSGSSSGSSSDGSSSQSGSSDSESGSESQSSESESD
M CHD-1	SVRNSSGESRSQSGDD-CGSASGSGSGSSSGSSSDGSSSQSGSSDSDSGSDSGSQSESESD
	*****
C CHD-1A	TSREKKQVQAKPPKADGSEFWKSSPSILAVQSAVLKQKQQQ---QKAASSDSGSEEDSS
M CHD-1	TSRENK-VQAKPPKVDGAEPWKSSPSILAVQSAVLKQKQQQ---QKAASSDSGSEEDSS
	*****
C CHD-1A	SSEDSADSSSETKCKKHKDEWQMSGSGSVSGTGSSESAEDGKSSCZESSESDYEPKN
M CHD-1	SSEDS-DDSSSGAKKCKHNDWQMSGSGSPQLGSDSESEERKSSCDGTESDYEPKN
	*****
C CHD-1A	KVRSRPPSRIPKPSGKKSTGQKQRLDSSEEEEDDEDYDKRGSRRQATVNVSYKEAEZ
M CHD-1	KVRSRPPSRIPKPSGKKSTGQKQRLDSSEEEEDDEDYDKRGSRRQATVNVSYKEAEZ
	*****
C CHD-1A	TKTDSDDLLEVCGEVDPQTEDEFETIEKFMDSRIGRKATGASTTIYAVEADGDPNAGF
M CHD-1	TKTDSDDLLEVCGEVDPQTEDEFETIEKFMDSRIGRKATGASTTIYAVEADGDPNAGF
	*****
C CHD-1A	KTKEHGEIQYLKWKGWSHIHNTWETETLKQONVRGMKLDNYKKKQDETKRWLNAS
M CHD-1	KTKEHGEIQYLKWKGWSHIHNTWETETLKQONVRGMKLDNYKKKQDETKRWLNAS
	*****
HUMAN	PEDVEYINCQQLTDDLEKQYQIVERI IABSNQKSAAGYPDYCKWQGLPYSECSWEDGA
C CHD-1A	PEDVEYINCQQLTDDLEKQYQIVERI IABSNQKSAAGYPDYCKWQGLPYSECSWEDGA
M CHD-1	PEDVEYINCQQLTDDLEKQYQIVERI IABSNQKSAAGYPDYCKWQGLPYSECSWEDGA
	*****
C CHD-1A	LIAXKQARIDEYFSRNQSKTTPFKDKCVLKQRPFRVALKQPSYIGGHELELRDYQLN
M CHD-1	LIAXKQARIDEYFSRNQSKTTPFKDKCVLKQRPFRVALKQPSYIGGHELELRDYQLN
	*****
C CHD-1A	GLNWLAEBSWCKGNSCIIADEMGLGKTIQTISFLNYLFHEBQLYGPFLLRVPLSTLTSWQR
M CHD-1	GLNWLAEBSWCKGNSCIIADEMGLGKTIQTISFLNYLFHEBQLYGPFLLRVPLSTLTSWQR
	*****
C CHD-1A	EIQTWAPQMNNAVYLGDIISRNMIRTHEWMBPQTKRLKFNILLTYEILLKDKSFLGGLN
M CHD-1	EIQTWASQMNNAVYLGDIISRNMIRTHEWMBPQTKRLKFNILLTYEILLKDKSFLGGLN
	*****
C CHD-1A	WAFIGVDEAERLKNDDSLYRTLIDFKSNRLLITGTPLQNSLKEWLSLHFIPEKPFSS
M CHD-1	WAFIGVDEAERLKNDDSLYRTLIDFKSNRLLITGTPLQNSLKEWLSLHFIPEKPFSS
	*****
C CHD-1A	WEDFEEHBGKREYGYASLHKELEPFLRRVKDVEKSLPAKVEQILRHEMSALQKQYYK
M CHD-1	WEDFEEHBGKREYGYASLHKELEPFLRRVKDVEKSLPAKVEQILRHEMSALQKQYYK
	*****
C CHD-1A	WILTRNYKALSCKSGSGTSGFLNIMMELKCCNHCYLIKPPDDNEFYNKQALQHLIRSS
M CHD-1	WILTRNYKALSCKSGSGTSGFLNIMMELKCCNHCYLIKPPDDNEFYNKQALQHLIRSS
	*****
C CHD-1A	GKLIILLDKLLIRLRERGNRVLIFSQVVRMLDILAEYLKYRQFPFQRLDGSIRKELRQAL
M CHD-1	GKLIILLDKLLIRLRERGNRVLIFSQVVRMLDILAEYLKYRQFPFQRLDGSIRKELRQAL
	*****

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C CHD-1A  
M CHD-1

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DHFNAGSEDFCFLSTRAGGLGINLASADTVVIFDSWNPQNDLQAQARAERIGQKKQV  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

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NIYRLVTKGSVEEDILERAQKKMVLDBLVIQRMDDTTGKTVLBTGSTPSSSTPFNKEZLSA  
NIYRLVTKGSVEEDILERAQKKMVLDBLVIQRMDDTTGKTVLBTGSTPSSSTPFNKEZLSA  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

ILKFGAEELFKPEPEXEEEPQEMDIDEILKRAETRENEGPGPLTVGDELLSQFKVANFSNM  
ILKFGAEELFKPEPEXEEEPQEMDIDEILKRAETRENEGPGPLTVGDELLSQFKVANFSNM  
ILKFGAEELFKPEPEXEEEPQEMDIDEILKRAETRENEGPGPLTVGDELLSQFKVANFSNM  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

DEDDIELEPEQNLNRWEEIPEEQWRRIEGXEQKELEEIYMLPRMNCARDISFNGNEZ  
DEDDIELEPERNSKNWEEIPEEQRRRLKEERQKELEEIYMLPRMNCARDISFNGNEZ  
DEDDIELEPERNSKNWEEIPEEQRRRLKEERQKELEEIYMLPRMNCARDISFNGNEZ  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

RCSRRRYSGSDSDSISERKRPKKRGRPTIPRENIGFSDAEIRRFIKSYKFGGPVER  
RRSRRRYSGSDSDSISERKRPKKRGRPTIPRENIGFSDAEIRRFIKSYKFGGPVER  
RRSRRRYSGSDSDSISERKRPKKRGRPTIPRENIGFSDAEIRRFIKSYKFGGPVER  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

LDAIARDAELVDKSETDLRLRGLZLVHNGCIKALNDNDFGQGRGTGGRFGVKGPTRLAGV  
LDAIARDAELVDKSETDLRLRGLZLVHNGCVKALKDSSGTERAGGLGKVKGPTRISGV  
LDAIARDAELVDKSETDLRLRGLZLVHNGCIKALNDNDFGQGRGTGGRFGVKGPTRISGV  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

QVNAKLVISHEEELAPLEKSIPSDPEERKRYVIPYHTKAHFIDWGEKDDSNLLIGIYE  
QVNAKLVIABEDELIPLEKSIPSDPEERKRYVIPYHTKAHFIDWGEKDDSNLLIGIYE  
QVNAKLVISHEEELAPLEKSIPSDPEERKRYVIPYHTKAHFIDWGEKDDSNLLIGIYE  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

YGYGSWEHIKMDPDLSTQKILPDOPDKKQAKQLQTRADYLIKLNKDLARKEAQRLAG  
YGYGSWEHIKMDPDLSTQKILPDOPDKKQAKQLQTRADYLIKLNKDLARKEAQRLAG  
YGYGSWEHIKMDPDLSTQKILPDOPDKKQAKQLQTRADYLIKLNKDLARKEAQRLAG  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

AGNSKRRKTRSKKATKAA  
AGGSKRRKTRAKSKAMKSIVKEEIKSDSSPLPEKSDDEDD---KLNDKPEKSDRS  
AGNSKRRKTRAKSKAMKSIVKEEIKSDSSPLPEKSDDEDD---KLNDKPEKSDRS  
\*\*\*\*\*

C CHD-1A  
M CHD-1

KKSVSDAPVHITASGEVPVIAEZEELDQKTFISICKERMFPVKAALKQDRPEKGLSER  
KKIPLLOTVPVHITATSEKVPVIAEZEELDQKTFISICKERMFPVKAALKQDRPEKGLSER  
\*\*\*\*\*

C CHD-1A  
M CHD-1

EQLEHTROCLIKIGDHITECLKEYSNPEQIKQWRKLNWIFVSKFTEFDARKLHKLYKHA  
EQLEHTROCLIKIGDHITECLKEYSNPEQIKQWRKLNWIFVSKFTEFDARKLHKLYKHA  
\*\*\*\*\*

C CHD-1A  
M CHD-1

KKROESQONSDQN-SNVATTHVIRNPDHERLKENTNHDSSRDSYSSDRHLSQYHDHFKD  
KKROESQONSDQN-SNVATTHVIRNPDHERLKENTNHDSSRDSYSSDRHLSQYHDHFKD  
\*\*\*\*\*

C CHD-1A  
M CHD-1

REQGDSEYKSDSRKRPYSSFSNGKDERWDHYRQDSRYSDREKHKLDHRSREHRPSL  
REQGDSEYKSDSRKRPYSSFSNGKDERWDHYRQDSRYSDREKHKLDHRSREHRPSL  
\*\*\*\*\*

C CHD-1A  
M CHD-1

EGGLKD-RCSDHRSBHDHRSBHDHRSSTPSTHIIINPPRDYRYSWQDLDERAASSGPRSP  
EGNLKDSRGSBHDHRSBHDHRSSTPSTHIIINPPRDYRYSWQDLDERAASSGPRSP  
\*\*\*\*\*

C CHD-1A  
M CHD-1

LDQSPYGSRSRSP-----FEHSAEHRSTPEHTWSSRKTQXKLMSLSSGTLFXP  
LDQSPYGSRSRSP-----FEHSAEHRSTPEHTWSSRKTQXKLMSLSSGTLFXP  
\*\*\*\*\*

C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A

LTXLERYGLDILSVAVLLLSRMQGLLSQKKNI FVFKVYAALCCCKCGTTF LRNRCILL  
LQGPQBCPPQTGSYYKTLFVKVVLGXTQIKLCLXMTXTLTCAVYSGONGGFI LFFFLVE  
NSQGLCSLSKATCLECTLRPPCRFSSQAXIFKPCYSCKLIARISPVCDQLXCLFHKQTNK  
QKTIKQNTTKPTNCKLLXINXMSFPFSGFWLFLSPTTQAFPSQSQYTYMFXNISMZ  
SECKNGELNILFBLVLLFYWILLBTCFWLFFYIFFFYXTVSVVIVVWNSENIPLXTVPWK  
AFQVHWFKRRCISIGZHFPTQISQDSLXIELFSLFNMGNVVKCAHQQLIFXKIMTLLTE  
LQCTLIVERXLLSDKLNKLPKKT

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644220" 9362630

**Figure 10.**

[illegible]

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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780 RVLIFSOMVRMLDILAAYLKRYQFFQRLDGSIKIGELRKQALDHFAEGS 829
| | | | | | | | | | : : | . . . : | | | | | . . . : | : : | | | . . :
3366 RVLIFSOMVRMLDILGDYLSIKGINFQRLDGTVPSPAQRRI SIDHFNSPDS 3415

830 EDFCFL LSTRAGGLGINLASADTVVIFDSDWNPNQNDLQAQARAHRIGQKK 879
: | | . | | | | | | | | | | . | | | | | | | | | | . | | | | | | | | | | .
3416 NDFVFLLSTRAGGLGINLMTADTVVIFDSDWNPNQADLQAMARAHRIGQKN 3465

880 QVNIYRLVTKG SVEEDILERAKKKMVL DDLVIQRMDTTGKT VLTGSTPS 929
: | : | | | . : . : | | : : | | | : | | : : . : | | . | . . . . .
3466 BVMVYRLVSKDTVEEVLERARKKMILEYAIISLGVDGNKYTKKNP.. 3513

930 SSTPFNKEELSAILKFGAEELFKPEGEQEPOEMDIDEILKRAETRENZ 979
| : | | | | | | | | : : | . . . : . . . : : : : : : : | : | : | . .
3514 .....NAGELSAILKFGAGNMFTATD.NQKKLEDNLDDVLNHAEDHVTT 3557

980 PG...PLTVGDELLSQFKVANFSNMDEDDIELEPERNSRNWEEIIPESQR 1026
| : . . . . : . : | . | . | . : : . . . : : : : | | | | | .
3558 PDLGESHLGGEEFLKQFEVTDY.....KADIDWDIIPEEEL 3594

1027 RRIEEEERQKELEE....IYMLPRMRNCAQOI..SFNGSE..... 1060
: : : : | . . . | | . . . : . . | . | . | . | . | . | . :
3595 KKLQDEEQKRKDEEYVKEQLEMNRDNALKKIKNSVNGDGTAANSDDSDD 3644

1061 ..GRRSRSSRYS GSDSDSITEKRKP KRGRPTIPR.ENIKGFSD...AE 1104
. . | . . . . : . : | | | . | . . : : : : : : : : | : | :
3645 DSTSRSSRRRARANDMSIGE...SEVRALYKAILKFGNLKEILDEL IAD 3691

1105 IRRFIKS YKFKGGPLERLDAVARDA.....ELVDKSETDLRRLGEL 1145
: | | : . : | : : : : . . : | . | . . | . : : | | . .
3692 GTLPVKSF EKYGETYDEMMEAARD CVHEEEKNRKEILEKLEKHATAYRAK 3741

1146 VENGCIKAL KD.NSSGQERAGGRLGVKGPTFRISGVQ.VNAKLVISHEE 1193
: . . | | | . : . . . . | : : . : . | . : | . : | . : : |
3742 LKSGEIKAE NQPKDNPLTRL SLKKREKKAVLFNFKG VKSLNAESLLSRVE 3791

1194 ELAPLHKS IPSD.PEERKRYVIPCHTKAA..HF DIDWGKEDDSNLLVGII 1240
: | | . . | | : . . . : : : . : : : : : | . : | . : | : :
3792 DLKYLKNLINSNYKD DPLKFSLGNNTPKPVQN WSSNWTKZEDEKLLIGVF 3841

1241 EYGYGSWEMI KM DPDL SLTQKILPDD..... 1266
. | | | | | . : : | | | : : | : : : :
3842 KYGYGSWTQIRDDP FLGITDKIFLNEVBNPVAKKSASSSDTTPTPSKK GK 3891

1267 ....PD KKPQAKQLQTRADYLIK LLNKDLARK.....EAQRLAGAGNS 1305
. . | | . : . | . | | | : : . : . | . : : : | : : . .
3892 GITGSSKKVPGAIB LGRRVDYLLSFLRGGLN TKSPSADIGSKKLPTGPSK 3941

1306 KRRKTRNKK NKMKASKIKEEIKSDSSQPSEKSD EDEE...EDNKVNEM 1352
| | : . . . . . | . . . . | . . : : . : . | . : . . : : : .
3942 KRQRKPANHS KSMTPEITSS EPANGPPSKRMKAL PKGAALINNTRLSPN 3991

1353 KSENKEKSKKI PLLDTPV HITATSEPVP ISEESEELBQKTFSVCKERM RP 1402
. . . | | | . : . : . : | . : | . : . . . | . : | . :
3992 SPTPPLKSKSV SRDNGTR...QSSNPSSGSA HEKEYDSMDEEDCRHTMSA 4037

1403 VKAALKQLDR PEKGLSEREQLEHBTROCLIKIGDHITECLK EYTNPEIQIQ 1452
: . . | | . | . : : | . : : : . : . : . : | | : | | : . .
4038 IRTSLKRLRR GGKSLDRKEWAK ILKTELTTIGNBI.E SQKGSSRKASPEK 4086

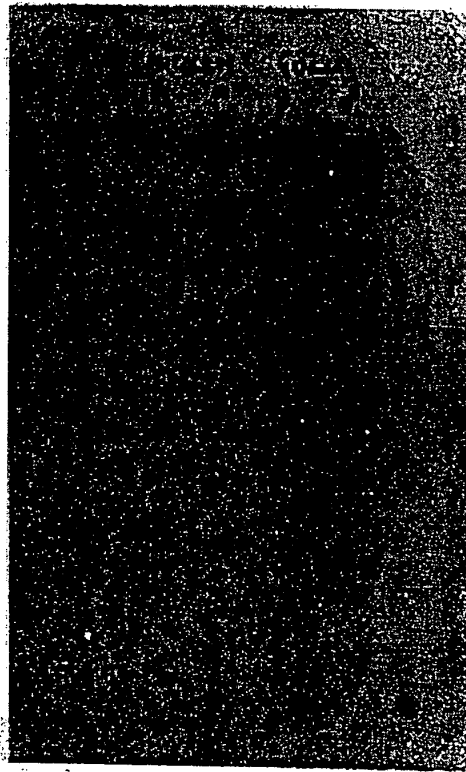
1453 WRKNLWIFV SKP..TEFDARKLEHKLYKHA IKRKQESQQ 1488
: | | : | : . . : . . . . | : | . | | | .
4087 YRKBLWSY SANFWPADVKSTLMAMY....DKITESOK 4120

```

[illegible]

CCHD	AVEAD	GDPNAGFEKSKELGE .IQYLIKWKWSHIBNTWETEET	LKQQNVKG MNKLDNYKK
MCHD	AVEAD	GDPNAGFERNKEPGD .IQYLIKWKWSHIBNTWETEET	LKQQNVRG NKKLDNYKK
YCHD	EKVVL	EKTVPDLNNCKE . N.YEFLIKWTDESHEBNTWETYES	IGQ . VRLKRLDNYCK
		**                ****          ** * * * * *	*     *     *
DHP1	EEEE	YAVEKIIDRRVRKGK.VEYLLKWKGYPETENTWEPEEN	LDCQDLIIQOY
HBP1	EDEEE	YVVEKVLDRRVVGKGQVEYLLKWKGFSSEBNTWEPEKN	LDCPELISEF
MMOD1	EEEE	YVVEKVLDRRVVGKG.VEYLLKWKGFSDEBNTWEPEEN	LDCPDLIAEF
MMOD2	AEPEE	FVVEKVLDRRVVNGK.VEYFLKWKGFTDADNTWEPEEN	LDCPELIEDF
	**	***      *****      *      *      *      *      *      *	***      **
DPC	PVDLV	YAAEKI IQKRVKKG.VEYR.VKWGWNQRYNTPENN	ILDRRLIDIY
MMOD3	VGEQV	FAAECILSKRLRKKG.LEYL VKWRGWSSKBNSWEPEEN	ILDPRLLLLAF
		*	*****

Figure 12.



361020\* E3E2/680

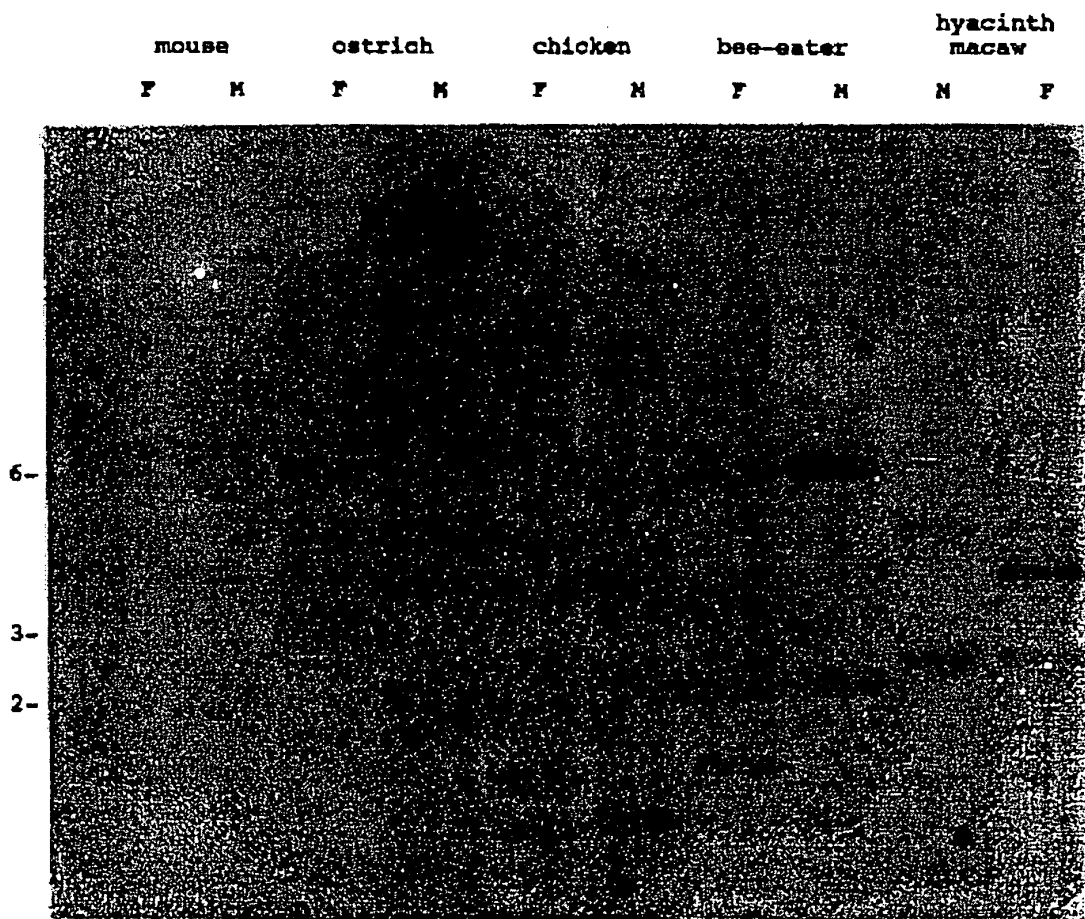
[illegible]

Figure 14.

MOUSE CHD1  
 CHICKEN CHD-1A  
 SPIX CHD-1A  
 CHICKEN CHD-W  
 SPIX CHD-W  
 HYACINTH CHD-W  
 P1  
 P3

AGA TAT TCT GGA TCT GAT AGT GAT TCA ATC TCG GAA  
 --- --- --- --- --- --- --- --- C --C --- A-A ---  
 --- --- --- --- --- --- --- --- C --C --- ---A ---  
 --- --- --- --- --- --- --- --- C --C --- ---A ---  
 --- --- --- --- --- --- --- --- C --C --- ---A ---  
 A TAT TCT GGA TCT GAT AGT GAY TC  
 AGA TAT TCC GGA TCT GAT AGT GA

MOUSE CHD1  
 CHICKEN CHD-1A  
 SPIX CHD-1A  
 CHICKEN CHD-W  
 SPIX CHD-W  
 HYACINTH CHD-W

AGG AAA CGG CCG AAG AAA CGT GGG CGA CCC CGC ACT  
 --A --- ---A --A --G --- --A A-- --T --A --C  
 --- --- ---A --A --G --- --A A-- --A --A ---  
 --A --- --A --A --A --- --A --- --A --A ---  
 --A --- --A --A --GA --- --A --- --A --A ---  
 --A --- --A --A --GA --- --A --- --A --A ---

MOUSE CHD1  
 CHICKEN CHD-1A  
 SPIX CHD-1A  
 CHICKEN CHD-W  
 SPIX CHD-W  
 P2  
 HYACINTH CHD-W  
 HYACINTH CHD-W

ATC CCT CGG GAG AAT ATT AAA GGA TTT AGT GAT GCG GAG  
 --T --- --A --A --- --- --- --- --- ---A ---  
 --T --- --A --A --- --A --- --- --- --- ---  
 --T --C --T --A --C --- --- --- --- ---A ---  
 --T --- --T --A --- --- --- --- --- ---  
 --- --- --- --- --- TTT CCT AAA TCG CTA CGT CT  
 ATT AGG CGG T --- --- --- --C --- --A --G



Figure 15.

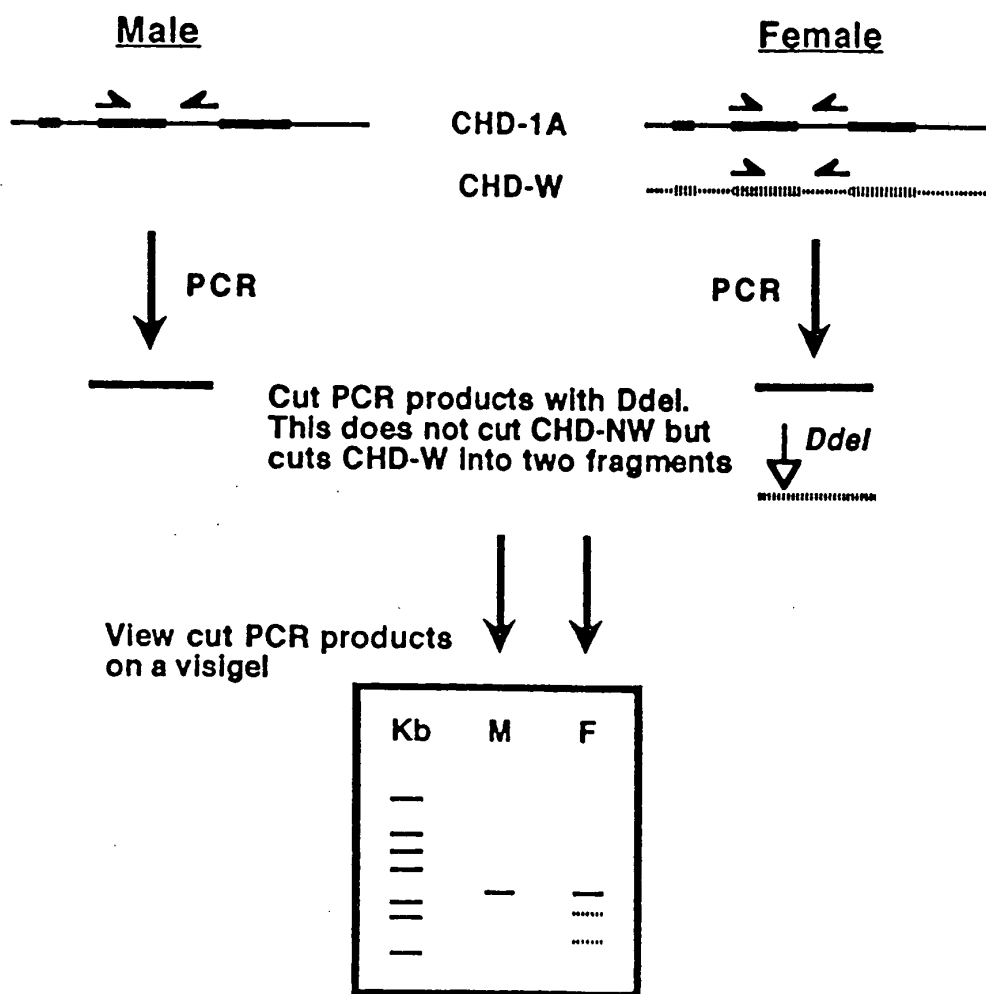


Figure 16.

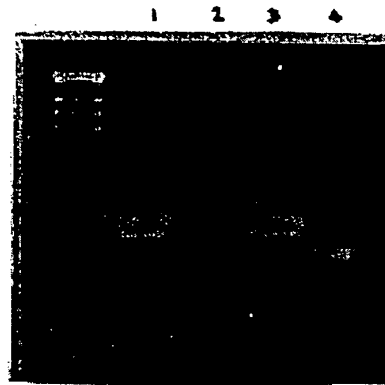


Figure 17.

